

**LIST OF REFERENCES CITED BY APPLICANT**  
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Application Number	10/566,953
Filing Date	January 31, 2006
First Named Inventor	Claes Gustafsson
Art Unit	1631
Examiner Name	To be assigned
Attorney Docket No.	11548-002-999

**U.S. PATENT DOCUMENTS**

*Examiner Initials	Cite No.	Document Number – Kind Code	Publication Date mm/dd/yyyy	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear
A01	US 2004/0072245 A1		04/15/04	Gustafsson <i>et al.</i>	
A02	US 2004/0161796 A1		08/19/04	Gustafsson <i>et al.</i>	
A03	US 2006/0205003 A1		09/14/06	Gustafsson <i>et al.</i>	
A04	US 2007/0239364 A1		10/11/07	Richard John Fox	
A05	US 2008/0050357		02/28/08	Gustafsson <i>et al.</i>	
A06					

**FOREIGN PATENT DOCUMENTS**

*Examiner Initials	Cite No.	Foreign Patent Document Country Code, Number, Kind Code (if known)	Publication Date mm/dd/yyyy	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T
B01						
B02						
B03						
B04						

**NON PATENT LITERATURE DOCUMENTS**

*Examiner Initials	Cite No.	Include name of the author (in CAPITAL LETTERS), (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T
C01	Adenot <i>et al.</i> , 1999, "Peptides quantitative structure-function relationships: An automated mutation strategy to design peptides and pseudopeptides from substitution matrices," Journal of Molecular Graphics and Modeling 17, 292-309.		
C02	Damborsky, Jiří, 1998, "Quantitative structure-function and structure-stability relationships of purposely modified proteins," Protein Engineering 11, 21-30.		
C03	Del Sol Mess <i>et al.</i> , 2003, "Automatic Methods for Predicting Functionally Important Residues," J. Mol. Biol. 326, 1289-1302.		
C04	Fariselli <i>et al.</i> , 2002, "Prediction of protein-protein interaction sites in heterocomplexes with neural networks," Eur. J. Biochem 269, 1356-1361.		
C05	Govindarajan <i>et al.</i> , 2003, "Systematic Variation of Amino Acid Substitutions for Stringent Assessment of Pairwise Covariation," J. Mol. Biol. 328, 1061-1069.		
C06	Hellberg <i>et al.</i> , 1986, "Peptide Quantitative Structure-Activity Relationships, a Multivariate Approach," J. Med. Chem 30, 1126-1135.		
C07	Jonsson <i>et al.</i> , 1993, "Quantitative sequence-activity models (QSAM)-tools for sequence design," Nucleic Acids Research 21, 733-739.		
C08	Lu <i>et al.</i> , 2001, "Predicting the reactivity of proteins from their sequence alone. Kazal family of protein inhibitors of serine proteinases," PNAS 98, 1410-1415.		

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EXAMINER SIGNATURE	/Shubo Zhou/	DATE CONSIDERED	06/20/2010
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	C09	Ness et al., 2001, "Molecular Breeding: The Natural Approach to Protein Design," Advances in Protein Chemistry 55, 261-292.	
	C10	Pierce et al., 2002, "Protein Design is NP-hard," Protein Engineering 15, 779-782.	
	C11	Sandberg et al., 1993, "Engineering multiple properties of a protein by combinatorial mutagenesis," Proc. Natl. Acad. Sci. 90, 8367-8371.	
	C12	Shaw et al., 2002, "Predicting Amino Acid Residues Responsible for Enzyme Specificity Solely from Protein Sequences," Biotechnology and Bioengineering 79, 295-300.	
	C13	Wrede et al. 1998, "Peptide Design Aided by Neural Networks; Biological Activity of Artificial Signal Peptidase 1 Cleavage Sites," Biochemistry 37, 3588-3593.	
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